additional mechanism that allows it to favor the higher rotation speed state. These findings are validated in a computational model of P. aeruginosa swimming and chemotaxis.

3285-Pos Board B440

Effect of Run and Tumble Time on Rheological Behavior of a Suspension of Escherichia Coli

Richa Karmakar, Ranjit Gulvady, Mahesh S. Tirumkudulu, K.V. Venkatesh.
IIT Bombay, Maharashtra, India.

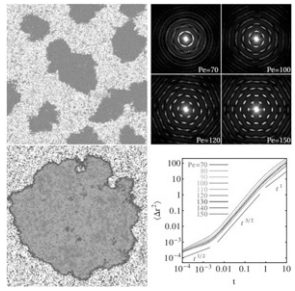
Microorganisms like microalgae and bacteria inject mechanical energy into the suspending fluid for their movement. Pusher-type bacterial cells such as Escherichia coli propel by rotating their flagella in a screw-like fashion. We measure the viscosity of a suspension of E. coli of different wild type and mutant strains at varying cell densities. The strains of E. coli differed in their run speeds, tumble time, and run time. The viscosity profile of the nonflagellated E. coli strain (BL21-DE3) increases linearly with cell density and agrees well with the prediction for a suspension of rod-shaped particles. Experiments were complimented with Small Angle Light Scattering (SALS) studies to observe the cell orientation in shear. The measured viscosity for all the strains were correlated with the chemotactic property of individual cells such as run speed, run time and tumble time. For smooth swimmers, we experimentally demonstrate the presence of instability at a critical cell density beyond which the viscosity decreases with increase in cell density.

3286-Pos Board B441

Structure and Dynamics of a Phase-Separating Active Colloidal Fluid

Gabriel S. Redner, Michael F. Hagan, Aparna Baskaran.
Brandeis University, Waltham, MA, USA.

We examine a minimal model for an active colloidal fluid in the form of self-propelled Brownian spheres that interact purely through excluded volume. Despite the absence of an aligning interaction, this system shows the signature behaviors of an active fluid, including anomalous number fluctuations and phase separation behavior. using simulations and analytic modeling, we quantify the phase diagram and separation kinetics. The dense phase is a unique material that we call an active solid, which exhibits the structural signatures of a crystalline solid near the crystal-hexatic transition point, but the rheological and transport properties associated with a viscoelastic fluid.



3287-Pos Board B442

Investigating Stator Dynamics of the Escherichia Coli Flagellar Motor

Laura E. Dickinson[1], Maarten M. van Oene[1], Francesco Pedaci[1], Bronwen Cross[1], Ren Lim[2], Richard M. Berry[2], Nynke H. Dekker[1].
[1]Delft University of Technology, Delft, Netherlands, [2]University of Oxford, Oxford, United Kingdom.

The bacterial flagellar motor (BFM) of the Escherichia Coli is an elegant molecular nano-machine that regulates bacterial motility. Powered by the proton-motive force, each motor generates mechanical torque via proton flux through numerous associated stator units that surround the rotor complex. These stator units freely diffuse in the cytoplasmic membrane and temporally engage with the BFM to rotate helical flagellar filaments and propel the bacterium to favorable environments. However, a fundamental understanding of stator dynamics of the BFM is still needed. We are employing a tweezer set-up that is capable of applying external torque to individual tethered E. Coli cells and therefore allows us to investigate mechanisms of the BFM. By adjusting the external load torque on the motor, we can physically control motor rotation, such as inducing forward rotation, backward rotation, and moments of stall to observe the behavior of the BFM with a temporal resolution of a few milliseconds. These results will further elucidate the dynamic role of stators in the BFM and in bacterial motility.

3288-Pos Board B443

Dynamic Conformational Changes of Flagellar Filament Observed by High-Pressure Microscopy

Masayoshi Nishiyama[1], Yoshiyuki Sowa[2].
[1]Kyoto University, Kyoto, Japan, [2]Hosei University, Tokyo, Japan.

The bacterial flagellar motor is a molecular machine that rotates a flagellum in both directions. CCW rotation allows the left-handed helical filaments to form a bundle that propels the cell smoothly, whereas CW rotation of a filament leads to change the shape of filament in right-handed helix and break the bundle, and inhibits smooth swimming of the cell, called a tumble. The switching in the helical structure is thought to be caused by directional mechanical actions arising from abrupt change of exerted torque by the motor rotation. Here, we show that application of pressure can also change the helical structure of flagellar filaments. The flagellar filaments in *E. coli* cells were fluorescently labeled, and then the images were acquired by using a high-pressure microscope [1, 2] with some modifications. We measured the diameter and pitch of the individual filaments and then classified them into 11 possible waveforms which are predicted from structural data. At 0.1 MPa (ambient pressure), all flagellar filaments formed left-handed helical structure (normal form). At 40 MPa, we found left-handed forms (normal and coiled forms) and right- (curly I (or II)). At 80 MPa, 80% flagellar filaments took curly I (or II) forms. After the pressure was released, most filaments returned to the initial left-handed structures. The application of pressure is thought to enhance the structural fluctuation and/or association of water molecules with the exposed regions of flagellin molecules, and results in switching the helical from left- to right-handed structure.

[1] Nishiyama M. and Y. Sowa. 2012. Microscopic Analysis of Bacterial Motility at High Pressure. *Biophys. J.* 102:1872-1880.
[2] Nishiyama M. and S. Kojima. 2012. Bacterial motility measured by a miniature chamber for high-pressure microscopy. *Int. J. Mol. Sci.* 13:9225-9239.

3289-Pos Board B444

Young's Modulus of *B. Subtilis* Cell Wall: Measuring and Modeling the Elasticity of Rod-Like Bacteria

Dmitri Vezenov, Michael J. Barrett.
Lehigh University, Bethlehem, PA, USA.

The peptidoglycan layer is the principle structural component of load baring cell wall in rod-like bacteria. As a polymer cross-linked into a rigid scaffold, peptidoglycan is responsible for characteristic shape of bacterial cells, their mechanical strength and durability. Atomic force microscopy (AFM) is an ideal tool to make highly precise measurements, to analyze multiple isolated cells, and to compare the mechanical properties between the individual bacterial cells. We can then investigate how the biology of the cells (deletion of specific proteins) or treatment and stresses to the cells (exposure to antibiotics) can affect the mechanics of their cell walls. Although there have been many studies of the mechanics of bacteria using AFM, many of them treat the force-indentation relationship in the terms of the standard Hertz model (i.e. approximate the cell as a uniform elastic solid). Of the few studies that treat the compression of a cell as the deformation of a thin elastic shell, none treat bacteria as a rod-like structure, which it resembles. We used large radii colloidal probes to obtain force-compression curves on multiple individual cells of wild type *B. Subtilis* and a mutant deficient in the protein mbl (Δmbl) that plays a key role in cell wall synthesis. To interpret the data in a quantitative manner, we developed a variety of analytical models for a rod-like elastic shell filled with incompressible fluid. We applied these models to describe the stretching of the cell wall and to calculate the Young's modulus of peptidoglycan in hydrated rod-like bacteria. Compared to wild type cells, the Young's modulus of the peptidoglycan in mutant bacterial cells is reduced by a third.

3290-Pos Board B445

Exploring the Mechanics of Magnetically Driven Motility in Magnetotactic Bacteria through Genetic Regulation

Mary E. Wilson[1], Lina M. Gonzaléz[1], Philip R. LeDuc[1], Warren C. Ruder[2].
[1]Carnegie Mellon University, Pittsburgh, PA, USA, [2]Virginia Tech, Blacksburg, VA, USA.

Magnetotactic bacteria guide themselves to optimal growth environments by a process termed magneto-aerotaxis, in which chains of intracellular magnetic nanoparticles, known as magnetosomes, orient along the Earth's geomagnetic field lines as a guide to efficiently locate oxygen-poor regions. From an external standpoint, this unique magnetotactic navigation system is regulated by key components: a magnetic nano-compass (magnetosome chain), a propulsion system (flagellar motility), and some magnetically-activated sensor (signal transduction). We hope to gain insight into these external systems by deconstructing the internal regulation of magnetotactic navigation from a genetics perspective. While genomic regions have been identified that encode magnetosome-related genes, little is known about how these genes regulate magnetosome production and how they interact with flagellar and cytoskeletal components to achieve guided motility. Here, we explore the genetic response of *Magnetospirillum magneticum* strain AMB-1 to an applied electromagnetic field as a means to identify genes activated by magnetic stimulation, focusing